In the Drawings

Applicants submit herewith proposed amendments to Figures 2, 3, 4, 5, 7A and 7B in red ink on separate sheets for the Examiners approval, pursuant to the provisions of 37 C.F.R. § 1.121 (d). Applicants respectfully request consideration and notification of approval by the Examiner of the proposed amendments to Figures 2, 3, 4, 5, 7A and 7B.

REMARKS

Introduction

Claims 1-31 are currently pending in this application. Upon entry of the amendments presented above, claims 21 and 22 will be pending in the instant application.

Restriction Requirement

The Examiner required restriction of the pending claims under 35 U.S.C. § 121 between one of the following inventions:

I. Claims 1-9 in part, drawn to pp32r1 DNA sequences, vector, and recombinant cell, classified in class 536, subclass 23.1;

II. Claims 1-9 in part, drawn to pp32r2 DNA sequences, vector, and recombinant cell, classified in class 536, subclass 23.1;

III. Claims 10-20, drawn to a method of diagnosing using pp32r1 DNA sequences, classified in class 435, subclass 6;

IV. Claims 10-20, drawn to a method of diagnosing using pp32r2 DNA sequences, classified in class 435, subclass 6;

V. Claims 21 and 22, drawn to antibody to pp32r1 protein, classified in class 530, subclass 387.9;

VI. Claims 21 and 22, drawn to antibody to pp32r2 protein, classified in class 530, subclass 387.9;

VII. Claims 23-28, drawn to an androgen-activated transcriptional promoter and at least one open reading frame of proteins, classified in class 536, subclass 23.1; and

VIII. Claims 29 and 30, drawn to screening method using the product of group VII, classified in class 435, ,subclass 4.

See Paper No. 15, pages 3-6. The Examiner further required election of one sequence falling within one of the above-identified inventions.

In response, Applicants hereby elect, without traverse, the invention of group five (V), represented by claims 21 and 22, drawn to an antibody to pp32r1 protein, classified in class 530, subclass 387.9. Applicants specifically note that the Examiner has not required an

election of species under group V, and accordingly Applicants assert that this response is fully responsive to the restriction requirement.

Sequence Listing

Applicants submit herewith a substitute "Sequence Listing" in paper copy and computer readable form (CRF). Applicants respectfully request entry of the substitute sequence listing into the instant application. The undersigned, hereby states that the content of the computer readable form of the "Sequence Listing" and the paper copy of the "Sequence Listing" submitted herewith are the same. The undersigned further submits that no new matter is introduced into the specification by way of entry of the substitute sequence listing. Support for the substitute "Sequence Listing" can be found throughout the application as originally filed, *inter alia*, at pages 26, 27, 33, 38-47, and Figures 2, 3, 4, 5, 7A and 7B.

The Examiner objected to the specification as allegedly failing to comply with the requirements of 37 C.F.R. §§ 1.821-1.825. Applicants have amended the specification herein to comply with the requirements of 37 C.F.R. §§ 1.821-1.825, and respectfully request reconsideration and withdrawal of the objections to the specification as allegedly failing to comply with the requirements of 37 C.F.R. §§ 1.821-1.825. A copy of the notice to comply mailed January 29, 2003, is included herewith.

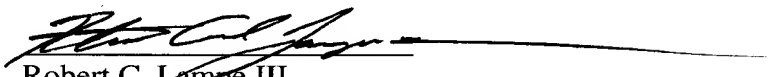
Conclusion

Applicants believe that consideration of the above remarks have placed this application in a condition for allowance. Early notification of a favorable consideration is respectfully requested.

Respectfully submitted,

HUNTON & WILLIAMS LLP

Dated: April 29, 2003

By: 

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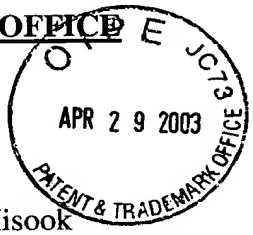
IN THE UNITED STATES PATENT AND TRADEMARK OFFICE



In re Patent Application of :)
)
Pasternack, G.R., *et al.*) Examiner: Yu, Misook
)
Serial No.: 09/591,500) Group Art Unit: 1642
)
Filed: June 12, 2000)

For: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY

Under Secretary of Commerce for Intellectual Property and
Director of the United States Patent and Trademark Office

Washington, D.C. 20231

Appendix A- Version with Markings to Show Changes Made to the Specification

In the paragraph located on page 26, lines 5-27:

--DNA from a bacteriophage clone containing pp32 cDNA sequences was digested with HindIII. Using routine methods, the restriction fragments were separated by agarose gel electrophoresis, transferred in alkaline buffer to positively charged nylon filters, and hybridized with probes that were selective for the 5' and 3' ends of the pp32 cDNA (Sambrook *et al.*). The 5' and 3' probes were prepared as described above except that the products of polymerase chain reactions (PCR) were used as templates for the labeling reactions (Saiki, *et al.*, Science, 239:487-491, 1988). One PCR product was a 249 base pair segment of pp32 cDNA containing nucleotides 32 through 279. It was the result of a reaction using a pp32 cDNA template and the primers

5'-TATGCTAGCGGGTTCGGGGTTTATTG-3' (SEQ ID NO: 41) and
5'-GATTCTAGATGGTAAGTTTGCGATTGAGG-3' (SEQ ID NO: 42)
(primer set A).

The other product was a 263 base pair segment of pp32 cDNA including nucleotides 677 through 938. It was the result of a reaction using a pp32 cDNA template and the primers

5'-GAATCTAGAAGGAGGAGGAAGGTGAAGAG-3' (SEQ ID NO: 43)

and

5'-CTATCTAGATTCAGGGGGCAGGATTAGAG-3' (SEQ ID NO: 44)

(primer set B).

The PCR reactions included 35 cycles of one minute denaturations at 95°C, one minute primer annealings at 50°C, and one minute extensions at 72°C (cycling program A). A 4.7 kb HindIII restriction fragment that hybridized with the 5' probe, but not with the 3' probe and a 0.9 kb HindIII fragment that hybridized with the 3' probe, but not with the 5' probe were subcloned into pBluescript (Gibco) by routine methods (Sambrook, et al.). The nucleotide sequences of both strands of purified plasmid DNA containing the inserts were determined by automated procedures (DNA Analysis Facility, Johns Hopkins University School of Medicine).--

In the paragraph located on page 26, line 28 extending to page 27, line 11:

--**Completion of Sequencing by Direct Sequencing of PCR Products.** Alignment of the sequences of the 4.7 and 0.9 kb HindIII restriction fragments with pp32 cDNA showed about 90% homologies between the 3' end of the 4.7 kb fragment and the 5' region of pp32 cDNA and the 5' end of the 0.9 kb fragment and the 3' region of the pp32 cDNA. There was an unaligned 199 base pair gap of pp32 cDNA sequence between the ends of the restriction fragments. Primers were designed to specifically anneal to relative pp32 sequences on both sides of the sequence gap. The primer sequences were

5'-GAGGTTTATTGATTGAATTCGGCT-3' (SEQ ID NO: 45) and

5'-CCCCAGTACACTTTTCCCGTCTCA-3' (SEQ ID NO: 46) (primer set C).

Polymerase chain reactions followed cycling program A with primer set C and pure bacteriophage DNA as a template. The 943 base pair products were shown by ethidium bromide staining agarose gels, extracted from excised fragments of low melt agarose (NuSieve) electrophoresis gels, and sequenced by automated procedures as described above.--

In the paragraph located on page 33, lines 5-19:

--**Analysis from freshly frozen human tissue and cell lines.** Total RNA is extracted from freshly frozen human tissues or human cancer cell lines and subjected to reverse transcription and polymerase chain reaction amplification with single set of primers capable of amplifying the entire coding region of the cDNA of all the three genes. A suitable set of primers is:

Upper: 5'GGGTTCGGGGTTTATTG3'- (SEQ ID NO: 47) This corresponds to bp32 to bp48 of the pp32 cDNA sequence (Genbank U73477)

Lower: 5'CTCTAATCCTGCCCCCTGAA3'- (SEQ ID NO: 48) This corresponds to bp919 of bp938 of the pp32 cDNA sequence (Genbank U73477)

The observed amplicon sizes with this primer set are pp32 – 907bp, pp32r1 – 889bp and pp32r2 – 900bp. The three cDNAs are distinguished from each other by restriction enzyme digestion with the following enzymes – EcoRI, Hind III and Xho I. The resultant digest is run on a 2.5% agarose gel to positively identify the three different cDNAs. The table below lists the sizes of the bands observed. The bolded numbers indicate the band sizes useful for identification of the three cDNAs.--

In Table 1:

--TABLE I

Position	Factor	Strand	Consensus Sequence
4	C	TTTCCT	PEA3
21	N	CAAGGTCA	ELP
23	N	AGGTCA	PPAR
32	C	CCCTAA	TBFl
41	N	CTTGGC	NF- 1 (-like proteins)
81	N	TAAACAC	Pit-1
82	N	AAACACA	HiNF-A
113	C	CTTCCC	c-Ets-2
118	N	CTATCA	GATA-1
122	N	CAGTTG	c-Myc
212	C	AATAAATA	TFIID
213	N	ATAAATA	ETF
247	N	TATCTA	NIT2
261	C	AAGGAA	c-Ets-2
262	B	AGGAAA	PEA3
283	C	TTTTTCTTTTTC	Hb (SEQ ID NO:49)
320	C	TTATAT	GAL4
333	N	TAAAAAA	TBP
349	N	TTATACATT	TBP
363	C	AAGGAA	c-Ets-2
394	C	TTTCTATA	TBP
398	N	TATAAA	TBP
398	N	TATAAA	TFIID
411	C	CTGAATT	Pit-1
420	N	TGTCCC	GR
423	C	CCCTAA	TBFl
434	N	TTCCTT	c-Ets-2
447	C	CTTCCC	c-Ets-2
514	N	TTATCTCT	GATA- 1
514	C	TTATCT	GATA-2
515	N	TATCTC	NIT2
537	N	TATGCA	EFII
553	N	AAGTCA	GCN4
608	N	TGACTA	GCN4
628	N	CCTCCCAAC	LyF- 1
640	N	TGTCCT	GR
648	N	TTAAAATTCA	1-Oct (SEQ ID NO:50)
648	N	TTAAAATTCA	4-Oct (SEQ ID NO:50)

Table 1 - Continued

649	N	TAAAAT	F2F
649	N	TAAAAT	Pit-1
661	N	TAAAAAA	TBP
673	N	CTTGGC	NF-1 (-like proteins)
725	N	AGGCGG	Spl
729	N	GGGCGG	ETF
729	N	GGGCGG	Spl
729	C	GGGCGG	Spl
741	N	AGGTCA	PPAR
793	N	TATAAATA	B factor
793	N	TATAAA	TBP
793	N	TATAAATA	TFIID
793	N	TATAAAT	TMF
794	N	ATAAATA	ETF
809	N	TTATCT	GATA-1
809	C	TTATCT	GATA-2
815	N	GGGTGTGG	TEF-2
826	C	CACATG	muEBP-C2
826	C	CACATG	TFE3-S
826	N	CACATG	USF
978	N	ATGTAAAACA	1-Oct (SEQ ID NO:51)
978	N	ATGTAAAACA	2-Oct (SEQ ID NO:51)
978	N	ATGTAAAACA	NF-IL-2A (SEQ ID NO:51)
1000	N	ATGTCAGA	CSBP-1
1006	N	GATTTC	H4TF-1
1034	C	TTTTCAT	Pit-1
1047	N	AAGATAAAACC	RVF (SEQ ID NO:52)
1048	C	AGATAA	GATA-1
1048	N	AGATAA	GATA-2
1049	N	GATAAA	TFIID
1083	C	GCCAAG	NF-1 (-like proteins)
1124	N	CGCCAT	UCRF-L
1163	C	GACCTG	TGT3
1307	N	CAGTCA	GCN4
1347	C	TGCATA	EFII
1373	C	AGAACA	AR
1373	N	AGAACAT	GR
1373	N	AGAACA	GR
1373	C	AGAACA	GR
1373	N	AGAACA	PR
1373	C	AGAACA	PR

Table 1 - Continued

1373	N	AGAACA	PR A
1373	C	AGAACA	PR A
1393	C	TCACTT	IFG-1
1393	C	TCACTT	IRF-2
1395	C	ACTTCCT	EIA-F
1423	N	TTATCT	GATA-1
1423	C	TTATCT	GATA-2
1424	N	TATCTA	NIT2
1452	N	TTACTC	GCN4
1471	N	TGGGTCA	C-Fos
1471	N	TGGGTCA	c-Jun
1471	N	TGGGTCA	ER
1496	N	TCTCTTA	c-Myc
1511	N	TATAAA	TBP
1511	N	TATAAA	TFIID
1549	C	TITGAA	TFIID
1568	C	AATGTATAA	TBP
1581	C	TTTGAA	TFIID
1590	C	AGATAA	GATA-1
1590	N	AGATAA	GATA-2
1591	C	GATAATTG	Dfd
1657	C	AGGACA	GR
1670	C	ATTTTA	F2F
1670	C	ATTTTA	Pit-1
1671	C	TTTTATA	B factor
1671	C	TTTTATA	Drl
1671	C	TTTTATA	En
1671	C	TTTTATA	TBP
1671	C	TTTTATA	TBP-1
1671	C	TTTTATA	TFIIA
1671	C	TTTTATA	TFIIB
1671	C	TTTTATA	TFIID
1671	C	TTTTATA	TFIIE
1671	C	TTTTATA	TFIIF
1671	C	TTTTATA	TRF
1672	C	TTTATA	TBP
1694	C	AATAAATA	TFIID
1695	N	ATAAATA	ETF
1733	N	AGGAAA	PEA3
1749	C	TTATAT	GAL4
1783	N	TAACTCA.	AP-1

Table 1 - Continued

1829	C	TAGATA	NIT2
1857	N	CGCCAT	UCRF-L
1875	N	TTCTGGGAA	IL-6 RE-BP
1895	N	TGACTA	GCN4
1899	N	TATTTAA	TBP
1942	N	ATATAA	GAL4
1985	C	TTTATA	TBP
1985	C	TTTATA	TFIID
2010	C	AATAAATA	TFIID
2011	N	ATAAATA	ETF
2058	C	TGCATA	EFII
2095	N	CAGTCA	GCN4
2146	C	AAGGAA.	c-Ets-2
2147	N	AGGAAA	PEA3
2190	N	AGGAAA	PEA3
2220	C	GGCACA	GR
2252	N	CCAATAG	gammaCAAT
2286	N	TGTGCC	GR
2292	N	ATGGGA	PTFl -beta
2314	N	TATGCA	EFII
2328	C	GGCACA	GR
2350	C	ATGATAAG	GATA-1
2351	N	TGATAAG	GATA-1
2363	N	GGGAAG	c-Ets-2
2367	N	AGCCACT	CP2
2369	C	CCACTGGGGA	AP-2 (SEQ ID NO:53)
2404	N	TAAAAT	F2F
2404	N	TAAAAT	F2F
2404	N	TAAAAT	Pit-1
2409	N	TTGTCATA	77+82K protein
2409	N	TTGTCATA	VETF
2415	N	TATCTA	NIT2
2451	C	TTTATC	TFIID
2452	N	TTATCT	GATA-1
2452	C	TTATCT	GATA-2
2486	N	CTCTCTCTCTCTC	GAGA factor (SEQ ID NO:54)
2644	N	AGGCGG	Spl
2658	N	ACAGCTG	GT-IIBalpha
2658	N	ACAGCTG	GT-IIBbeta
2709	C	GGCCAGGC	AP-2
2723	N	TGA4CT	GR

Table 1 - Continued

2731	C	TGACCT	PPAR
2731	C	TGACCTCA	URTF
2753	N	CTTGGC	NF-1 (-like proteins)
2818	C	TGATGTCA	AP-1
2818	C	TGATGTCA	c-Fos
2818	C	TGATGTCA	c-Jun
2818	C	TGATGTCA	CREB
2845	N	GGGAAG	c-Ets-2
2858	N	AGATAG	GATA-1
2858	C	AGATAG	GATA-1
2864	C	AGTTCA	GR
2899	N	ATATAA	GAL4
2900	N	TATAAAA	B factor
2900	N	TATAAAA	Drl
2900	N	TATAAAA	En
2900	N	TATAAAA	TBP
2900	N	TATAAA	TBP
2900	N	TATAAAA	TBP-1
2900	N	TATAAAA	TFIIA
2900	N	TATAAAA	TFIIB
2900	N	TATAAAA	TFIID
2900	N	TATAAAA	TFIIE
2900	N	TATAAAA	TFIIF
2900	N	TATTAAAA	TRF
2921	C	TTTGAA	TFIID
2924	C	GAAATC	H4TF-1
2930	C	CATTAG	IsI-1
2948	C	TGTACA	GR
2948	C	TGTACA	PR
2948	C	TGTACA	PR A
2964	C	ATTTGAGAA	VITF
3030	N	AGTG'TTCT	GR
3032	N	TGTTCT	AR
3032	N	TGTfCT	GR
3032	C	TGTfCT	GR
3032	N	TGTTCT	PR
3032	C	TGTTCT	PR
3032	N	TGTTCT	PR A
3032	C	TGTTCT	PR A
3104	C	GGATTATT	TII
3106	C	ATTATTAA	AFP1

Table 1 - Continued

3111	N	TAAAAT	F2F
3111	N	TAAAAT	Pit-1
3125	C	ATTTTA	F2F
3125	C	ATTTTA	Pit-1
3142	N	TGTGAT	GR
3169	N	GTTTTATT	HOXD10
3169	N	GTTTTATT	HOXD8
3169	N	GTTTTATT	HOXD9
3175	C	TTTGAA	TFIID
3185	N	TTGCTCA	Zta
3206	N	GATTTC	H4TF-1
3212	N	AGGAAA	PEA3
3238	C	ATTTTA	F2F
3238	C	ATTTTA	Pit-1
3256	C	TTTGAA	TFIID
3266	N	TTGCTCA	Zta
3320	C	ATTTTA	F2F
3320	C	ATTTTA	Pit-1
3358	N	ATGGGA	PTF1-beta
3360	C	GGGACA	GR
3440	C	CACTCA	GCN4
3460	C	TTTCCT	PEA3
3483	N	GACACA	GR
3491	C	TTTCCT	PEA3
3495	N	CTAATG	IsI-1
3523	C	AGAACA	AR
3523	N	AGAACA	GR
3523	C	AGAACACT	GR
3523	C	AGAACA	GR
3523	N	AGAACA	PR
3523	C	AGAACA	PR
3523	N	AGAACA	PR A
3523	C	AGAACA	PR A
3538	C	TTTATC	TFIID
3539	N	TTATCT	GATA-1
3539	C	TTATCT	GATA-2
3551	N	TGAGTG	GCN4
3569	C	TCCCAT	PTF 1 -beta
3594	N	TTAGGG	TBF1
3653	C	CCTGCTGAA	LyF-1
3668	N	CTCATGA	1-Oct

Table 1 - Continued

3668	N	CTCATGA	2-0ct
3668	N	CTCATGA	Oct-2B
3668	N	CTCATGA	Oct-2B
3668	N	CTCATGA	Oct-2C
3679	C	TGTGTAA	Zta
3685	C	AGAACT	GR
3712	C	TTTCCT	PEA3
3713	N	TTCCTT	c-Ets-2
3717	N	TTGCTCA	Zta
3727	C	AAAACATAAAT	ssARS-T (SEQ ID NO:55)
3749	N	TAAAAAA	TBP
3784	C	CACTCA	GCN4
3791	C	ATTTTA	F2F
3791	C	ATTTTA	Pit-1
3815	N	TATCTA	NIT2
3829	C	TAGATA	NIT2
3859	C	AGAACA	AR
3859	N	AGAACAG	GR
3859	N	AGAACA	GR
3859	C	AGAACA	GR
3859	N	AGAACA	PR
3859	C	AGAACA	PR
3859	N	AGAACA	PR A
3859	C	AGAACA	PR A
3860	N	GAACAG	Lva
3877	C	ATCACA	GR
3886	N	TGAGTCA	AP-1
3886	C	TGAGTCA	AP-1
3886	C	TGAGTCA	c-Fos
3886	C	TGAGTCA	c-Jun
3886	C	TGAGTCA	Fral
3886	C	TGAGTCA	NF-E2
3887	C	GAGTCA	GCN4
3931	N	AGATAG	GATA-1
3931	C	AGATAG	GATA-1
3960	N	TTGGCA	NF-I/L
3965	C	ATTTTA	F2F
3965	C	ATTTTA	Pit-1
4026	N	TATTTAA	TBP
4037	N	TCTGAT	GR
4040	N	GATGCAT	Pit-1

Table 1 - Continued

4042	C	TGCATA	EFII
4079	N	TTCAAAG	SRY
4079	N	TTCAAAG	TCF-1A
4079	N	TTCAAA	TFIID
4079	N	CAGGTC	TGT3
4140	N	TGATTCA	AP-1
4140	C	TGATTCA	AP-1
4140	N	TGATTC	GCN4
4164	N	GGGAGTG	p300
4205	C	AGATAA	GATA-1
4205	N	AGATAA	GATA-2
4219	C	TTAGTCAC	AP-1
4219	C	TTAGTCA	AP-1
4219	C	TTAGTCAC	c-Fos
4219	C	TTAGTCAC	c-Jun
4219	C	TTAGTCA	c-Jun
4219	C	TTAGTCA	Jun-D
4220	C	TAGTCA	GCN4
4271	N	TGTTCT	AR
4271	N	TGTTCT	GR
4271	C	TGTTCT	GR
4271	N	TGTTCT	PR
4271	C	TGTTCT	PR
4271	N	TGTTCT	PR A
4271	C	TGTTCT	PR A
4280	C	TGACCCA	c-Fos
4280	C	TGACCCA	c-Jun
4280	C	TGACCCA	ER
4292	C	CTTATCAG	GATA-1
4292	C	CTTATCA	GATA- 1
4361	N	TTCAAAG	SRY
4361	N	TTCAAAG	TCF-1A
4361	N	TTCAAA	TFIID - -

In Table 2:

--TABLE 2

COMPARISON OF ALL PROTEIN SEQUENCES

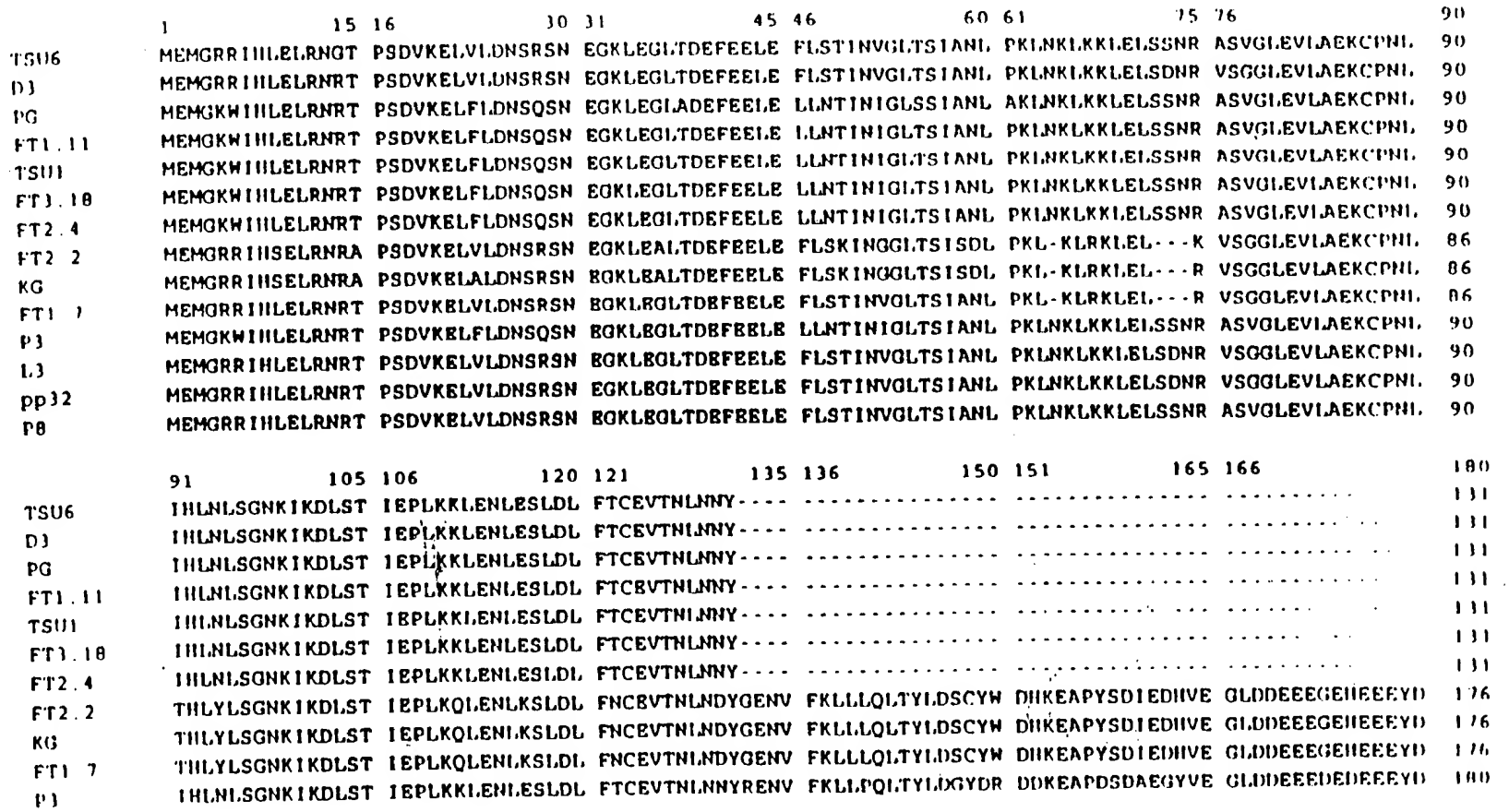


Table 2 - Continued

	91	105	106	120	121	135	136	150	151	165	166	180
L3	THLNLSGNKIKDLST		IEPLKKLENLKSLKL		FNCEVTNLNDYRENV		FKLLPQLTYLDGYDR		DDKEAPDSDAEGYVE		GLDDEEEDEDEEEYD	180
pp32	THLNLSGNKIKDLST		IEPLKKLENLKSLDL		FNCEVTNLNDYRENV		FKLLPQLTYLDGYDR		DDKEAPDSDAEGYVE		GLDDEEEDEDEEEYD	180
P8	THLNLSGNKIKDLST		IEPLKKLENLKSLDL		SNCEVTNLNDYRENV		FKLLPQLTYLDGYDR		DDKEAPDSDAEGYVE		GLDDEEEDEDEEEYD	180

	181	195	196	210	211	225	226	240	241		
TSU6	----------		----------		----------		----------		----------	131	(SEQ ID NO: 28)
D3	----------		----------		----------		----------		----------	131	(SEQ ID NO: 37)
PG	----------		----------		----------		----------		----------	131	(SEQ ID NO: 38)
FT1.11	----------		----------		----------		----------		----------	131	(SEQ ID NO: 29)
TSU1	----------		----------		----------		----------		----------	131	(SEQ ID NO: 29)
FT3.18	----------		----------		----------		----------		----------	131	(SEQ ID NO: 29)
FT2.4	----------		----------		----------		----------		----------	131	(SEQ ID NO: 29)
FT2.2	EDAQVVEDEEGEEEE		EEGEEEDVSGGDEED		EEGYNDGEVDGEEDE		EELGEEERGQKRK--		----------	234	(SEQ ID NO: 39)
KG	EDAQVVEDEEGEEEE		EEGEEEDVSGGDEED		EEGYNDGEVDGEEDE		EELGEEERGQKRK--		----------	234	(SEQ ID NO: 4)
FT1.7	EDAQVVEDEEGEEGE		EEGEEEDVSGGDEED		EEGYNDGEVDDEEDE		EELGEEERGQKRKRE		PEDEGEDDD	245	(SEQ ID NO: 5)
P3	EDAQVVEDEEDEDEE		EEGEEEDVSGEEEED		EEGYNDGEVDDEEDE		EELGEEERGQKRKRE		PEDEGEDDD	249	(SEQ ID NO: 31)
L3	EDAQVVEDEEDEDEE		EEGEEEDVSGEEEED		EEGYNDGEVDDEEDE		EELGEEERGQKRKRE		PEDEGEDDD	249	(SEQ ID NO: 40)
pp32	EDAQVVEDEEDEDEE		EEGEEEDVSGEEEED		EEGYNDGEVDDEEDE		EELGEEERGQKRKRE		PEDEGEDDD	249	(SEQ ID NO: 40)
P8	EDAQVVEDEEDEDEE		EEGEEEDVSGEEEED		EEGYNDGEVDDEEDE		EELGEEERGQKRKRE		PEDEGEDDD	249	(SEQ ID NO: 30)

TSU6 and TSU1 from TSU cell line; D3 from DU-145 cell line; P3 and P8 from PC-3 cell line; FT1, FT2 and FT3 from patient carcinoma; LE from LNCAP; KG from placenta--